	GGCACGAGTG TGCCTAACAG AGAAAGAGAG ACCGATAGCC TCCTCATTCA CTATGGCGAT	60
	CCGATCGCCA GCTTCGCTGC TGTTATTTGC GTTTCTGATG CTTGCGCTCA CAGGAAGACT	120
5	GCAGGCCGGG CGCAGCTCGT GCATTGGCGT CTACTGGGGA CAAAACACAG ACGAGGGAAG	180
	CTTAGCAGAT GCTTGTGCCA CAGGCAACTA CGAATACGTG AACATCGCCA CCCTTTTCAA	240
10	GTTTGGCATG GGCCAAACTC CANAGATCAA CCTCGCCGGC CACTGTGACC CTCGGAACAA	300
	CGGCTGCGCG CGCTTAAGCA GAGAAATCCA GTCCTGCCAG GAGCGTGGAG TCACGGTGAT	360
	GCTCTCCATC GGAGGTGGCG GGTCTTATGG CCTGAGTTCC ACCGAAGACG CCAAGGACGT	420
15	GGCGTCATAC CTCTGGCACA GTTTCTTGGG TGGTTCTGCT GCTCGCTACT CTCGACCCCT	480
	CGGGGATGCG GTTCTGGATG GCATANACTT CAACATCNCC GGAGGGAGCA CAGAACACTA	540
20	TGATGAACTT GCCGCTTTCC TCAAGGGCTA CNACGAACAG GAAGCCGGAA CGAAAAAANT	600
	TTTACTTGAA TGCTGCTCCC NCANTGTCCT TTCCCGGATT ACTGGCTTGG CACCCACTCA	660
	NAAAANATCT CTTCCNACTT CCNTGTGGGT TGCANTTCCT CCAANAACCC TTCCTTGCCN	720
25	TTTCTCCCCA AAACCTATCC ATCTTGCAAT TCCTTTCACA AATTGGGTCN TNTCCNTCCC	780
999 1999	NGCCCCNAAA ACTTTTCCC TNGGGCTCC	809
1) 1] 30	(2) INFORMATION FOR SEQ ID NO: 48:	
35	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 809 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: unknown 	
Service Charles	(ii) MOLECULE TYPE: cDNA	
40	(vii) IMMEDIATE SOURCE: (B) CLONE: U-D86	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:	
	GGCACGAGCC ACAAGCTTGC CTTTGGTTGT GCCTAACAGA GAGAGAGAGA GAGACAGACC	60
50	GATAGCCTCC TCATTCACTA TGGCGATCCG ATCGCCAGCT TCGCTGCTGT TATTTGCGTT	120
50	TCTGATGCTT GCGCTCACAG GAAGACTGCA GGCCCGGCGC AACTCATGCA TTGGCGTCTA	180
	CTGGGGACAA AAGACAGACG AGGGAAGCTT AGCAGATGCT TGTGCCACAG GCAACTACGA	240
55	ATACGTGAAC ATCGCCACCC TTTTCAAGTT TGGCATGGGC CAAACTCCAG AGATCAACCT	300
	CGCTAGCCAC TGTGACCCTC AGAACAACGG CTGCGCGCGC TTAAGCAGCG AAATCCAGTC	360
60	CTGCCAGGAG CGTGGAGTCA AGGTGATGCT CTCCATCGGA GGTGGCGGGT CTTATGGCCT	420
υυ	GAGTTCCACC GAAGACGCCA AGGACGTGGC GTCATACCTC TGGCACAGTT TCTTGGGTGG	480
	TTCTGCTGCT CGCTACTCTC GACCCCTCGG GGATGCGGTT CTGGATGGCA TAAACTTCAA	540
65	CATCNCCGGA GGGAGCACAG AACACTATGA TGAACTTGCC GCTTTCCTCA AGGGCTACAA	600
	CGANCAGGAA GCCGGAACGA AAAAAGTTCA CTTGAATGCT GCTCCCCANT GTCTTTCCCG	660
70	GATTACTGGC TTGGCAACGC NCTCCAAAAC AAATCTCTTC CACTTCCTGT GGGTGCANTC	720

CTCCACAAAC CTTCNTGCAT TCTCCCCAAA CCTATCAATC TTGCNAAATG CGTTCAACAA 780

	TTNGGGTCTT TTCATCCCCG CCCAAAACT	809
_	(2) INFORMATION FOR SEQ ID NO: 49:	
5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 785 base pairs (B) TYPE: nucleic acid	
10	(C) STRANDEDNESS: single (D) TOPOLOGY: unknown	
	(ii) MOLECULE TYPE: cDNA	
15	(vii) IMMEDIATE SOURCE: (B) CLONE: U-D90	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:	
	GGCACGAGGA GAGACCGATA GCCTCCTCAT TCACTATGGC GATCCGATCG CCAGCTTCGC	60
25	TGCTGTTATT TGCGTTTCTG ATGCTTGCGC TCACAGGAAG ACTGCAGGCC GGGCGCAGCT	120
23	CGTGCATTGG CGTCTACTGG GGACAAAACA CAGACGAGGG AAGCTTAGCA GATGCTTGTG	180
	CCACAGGCAA CTACGAATAC GTGAACATCG CCACCCTTTT CAAGTTTGGC ATGGGCCAAA	240
30	CTCCAGAGAT CAACCTCGCC GGCCACTGTG ACCCTCGGAA CAACGGCTGC GCGCGCTTAA	300
	GCAGAGAAAT CCAGTCCTGC CAGGAGCGTG GAGTCACGGT GATGCTCTCC ATCGGAGGTG	360
35	GCGGGTCTTA TGGCCTGAGT TCCACCGAAG ACGCCAAGGA CGTGGCGTCA TACCTCTGGC	420
33	ACAGTTTCTT GGGTGGTTCT GCTGCTCGCT ACTCTCGACC CCTCGGGGAT GCGGTTCTGG	480
	ATGGCATANA CTTCAACATC GCCGGAGGGA GCACAGAACA CTATGATGAA CTTGCCGCTT	540
40	TCCTCAAGGC CTACAACGAG CAGGAAGCCG GAACGAAAAA AGTTTACTTG AATTGCTGCT	600
	CCGCANTATC CTTTCCNGAT TACTGGCTTG GCAACNCNCT CCAAAAAANA TCTCTTCCAC	660
45	TTCCTGTTGG GTGCAGTTCT TCCAANAACC CNTTCNTGCC ATTTCTCCCC AAAACGCTTT	720
4 <i>5</i>	CCATCTTTGC AAATGCCTTT CAACAATTGG GGTCTTGTTC CNNCCCTGCC CCAAAAACTG	780
	TTCCT	785
50	(2) INFORMATION FOR SEQ ID NO: 50:	
55	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 813 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: unknown	
	(ii) MOLECULE TYPE: cDNA	
60	(V1i) IMMEDIATE SOURCE:	
	(B) CLONE: U-D93	
65	(vi) anarona anarona	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:	
70	GGCACGAGCG ATAGCCTCCT CATTCACTAT GGCGATCCGA TCGCCAACTT CGCTGCTGTT	60
, U	ATTTGCGTTC CTGATGCTTG CGCTCACGGG AAGACTGCAG GCCCGGCCCA GCTCATGCAT	120

180

TGGCGTCTAC TGGGGACAAA ACACCGACGA GGGAAGCTTA GCAGATGCTT GTGCCACAGG

	CAACTACGAT TACGTGAACA TCGCCACCCT TTTCAAGTTT GGCATGGGCC AAACTCCAGA	240
5	GATCAACCTC GCCGGCCACT GTGACCCTCG GAACAACGGC TGCGCGCGCT TGAGCAGCGA	300
	AATCCAGTCC TGCCAGGAGC GTGGCGTCAA GGTGATGCTC TCCATCGGAG GTGGCGGGTC	360
10	TTATGGCCTG AGTTCCACCG AAGACGCCAA GGGAAGTAGC GTCATACCTC TGGCACAGTT	420
10	TCTTGGGTGG TTCTGCTGCT CGCTACTCGA GACCCCTCGG GGATGCGGAA CTGGATGGCA	480
	TANACTTCAA CATCGCCGGA GGGAGAACAG AACACTATGA TGAACTTGCC GCTTTCCTCA	540
15	AGGCCTACAA CGANCAGGAA GCCGGAACNA AAAAAGTTCA CTTGAATTGC TGCTCCGCAG	600
	TGTCCTTTCC CGGATTACTG GCTTGGCAAC GCACTCAGAA CANATCTCTT CNACTTCCTG	660
20	TGGGTGCAAT TTCCTCCACA ANCCTTCCNT GCCATTTCTC CCAAAAAGCT ATCNATCTTG	720
20	CAAATGCGTT CNACAATTGG GTCTTTTCCA NCCTGCNCAA AACTGTTCCT TGGGCTCCCG	780
F5 25	CTGCCCCTGA AGGTGCNCCA ATTGGTGGCT NCT	813
1 25	(2) INFORMATION FOR SEQ ID NO: 51:	
y mone, front front and	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 819 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: unknown	
= 1 = 1	(ii) MOLECULE TYPE: cDNA	
35 ming over shift and ming shift and	(vii) IMMEDIATE SOURCE: (B) CLONE: U-D61	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:	
	GGCACTCAGG AACTCCAACA TCCAAGTCCT GTTGGATGTC CCCCGATCCG ACGTGCAGTC	60
45	ACTGGCCTCC AATCCTTCGG CCGCCGGCGA CTGGATCCGG AGGAACGTCG TCGCCTACTG	120
	GCCCAGCGTC TCCTTTCGAT ACATAGCTGT CGGAAACGAG CTGATCCCCG GATCGGATCT	180
	GGCGCAGTAC ATCCTCCCCG CCATGCGCAA CATCTACAAT GCTTTGTCCT CGGCTGGCCT	240
50	GCAAAACCAG ATCAAGGTCT CGACCGCGGT CGACACGGGC GTCCTCGGCA CGTCCTACCC	300
	TCCCTCCGCC GGCGCCTTCT CCTCCGCCGC CCAGGCGTAC CTGAGCCCCA TCGTGCAGTT	360
55	CTTGGCGAGT AACGGAGCGC CGCTCCTGGT CAATGTGTAC CCTTATTTTA GCTACACCGG	420
	CAACCCGGGA CAGATCTCGC TGCCCTACGC CCTGTTCACG GCCTCCGGCG TCGTCGTGCA	480
	GGATGGGCGA TTCANCTATC AGAACCTGTT CGACGCCATC GTCGACGCGG TCTTCGCGGC	540
60	GCCTGGAAAA AATGGGAAGG GCGAACGTGG CGGTGGTGGT GTCCGAAAAC GGGTGGCCGT	600
	CCGCGGGCGG AAGAACCCNA AACNAACACC ANCAACNCCG CCGGAANTTT CAACCANAAC	660
65	TTGATCAGGC ATGTTNGGCG GAAGAACCCC AAGGAAAACC AGGGAAGGAA ATCAAGGCTT	
	CNTNTTCCAA AANTTTCCAC CAAAAACCNA AAGGTGGANG GATCCAACAA AACTTTGGCC	
	TGTTTTATCC CAANNAACAN CCCNTCTTAC CNAATAACT	819
70	(2) INFORMATION FOR SEQ ID NO: 52:	